Graphical models for estimating dynamic networks

Abbruzzo, Antonio

Stellingen
behorende bij het proefschrift

Graphical models for estimating dynamic networks

door
Antonino Abbruzzo

I. A genomic network is only a metaphor for genetic regulation and signalling (Chapter 1).

II. Graphical models are only one formalization of a network, albeit a powerful one (Chapter 2).

III. Colouring graphs is fun, but computationally difficult (Chapter 3).

IV. Sparsity is not only computationally useful, but also represents our current best knowledge of genomic interaction (Chapter 2).

V. Networks are too often seen as state entities. The overall aim of this thesis is to animate them (Chapter 3-5).

VI. Popularly, interactions are seen as first moment properties. Surprisingly, Gaussian graphical models show that it is easier to implement them via second moments (Chapter 2).

VII. On the side of having destroyed many pension plans, the Gaussian Copula is particularly useful for dealing with non-normal genomic data (Chapter 4).

VIII. Our biology is resistant to change both neurologically as well as genetically. That is why in (Chapter 5.1) we like the model that infer only slowly changing genomic networks.

IX. Scale-free networks are obviously rubbish models for the genomic reality, but can serve as prior for doing inference (Chapter 5.2).

X. "....."
(Non-observed information make inference a lot harder) (Chapter 5.3).